REMARKS

Claims 25-28, 38, 39, 44, 47, 51, 52, and 58-60 are pending and rejected.

Claim 52 has been amended to recite the endogenous nucleotide sequence encoding the polypeptide of SEQ ID NO:24 comprises SEQ ID NO:23. Support for this amendment is in the specification on page 9, lines

Claim 60 has been amended to recite, wherein the endogenous nucleotide sequence is a DNA molecule comprising the nucleotide sequence of SEQ ID NO:23 and comprises a mutation.

No new matter has been added by these amendments.

Claim Objections

Claim 60 is objected to for reasons in the Office Action. Claim 60 has been amended to recite that the endogenous sequence of the protein encoding region is SEQ ID NO:23 and comprises a mutation.

Claim Rejections under 35 USC § 112, second paragraph

Claims 52 is rejected under 35 USC § 112, second paragraph as allegedly being indefinite for failing to particularly point out and distinctly claim the invention for using the word "endogenous" to describe SEQ ID NO:23.

Applicants respectfully disagree with this rejection, however, claim 52 has been amended to recite that SEQ ID NO:23 is the nucleotide sequence encoding the endogenous protein encoding region.

Claims 25-28, 38, 39, 44, 47, 58 and 59 remain and claims 51, 52 and 60 are rejected under 35 USC § 112, second paragraph for allegedly being indefinite for failing to particularly point out and distinctly claim the invention. The Office Action alleges that "the specification does not describe any transgenic plant comprising any kind of mutation in an endogenous nucleotide sequence encoding SEQ ID NO:24, or any regulatory region thereof." The Office Action sites *Fiers v. Revel* for the proposition that "an adequate written description of a DNA requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it; what is required is a description of the DNA itself."

Applicants respectfully disagree with this rejection. The specification as filed does provide a written description of the invention. Firstly, "the DNA is described itself" as SEQ ID NO:23 is the DNA sequence for the amino acid sequence of SEQ ID NO:24. The specification does describe the gene when it provides the Sequence of

SEQ ID NO:23. Page 16-17 of the specification describes the sequence listing and provides a description for SEQ ID NOS: 23 and 24.

Second, the present application differs from the case of *Fiers*. In *Fiers*, the application lacked any actual DNA sequence of the gene in question. The present application provides the gene sequence in SEQ ID NO:23.

Lastly, a transgenic plant with a mutation in SEQ ID NO:23 and the protein of amino acid sequence SEQ ID NO:24 is described in Example 5 as explained in the response file previously. While Example 5 was written in the present test, there is a Table of data (Table 3) which describes the results of the experiment of Example 5. The level of detail provided for the results, particularly Table 3, demonstrates that the experiments were actually carried out and that such exact data would not have been provided if the example was prophetic. Applicants submit that one skilled in the art would recognize that this level of detail would not be used in a prophetic statement. In table 3, it states that in the Homozygous F3, which were F3 plants from the S11.13-34 x 8Z-2 F3 hybrid homozygous for the 35S-GFP and S11.13-34 T-DNAs. This is the homozygous mutant having the "gene encoding the RNase D domain related protein with T-DNA insertion. mRNA is not expressed." The data in columns 4 and 5 show that 0/36 plants exhibited PTGS.

Example 2, entitled "Insertion mutagenesis in a nucleotide sequence encoding a polypeptide comprising a RNase D related domain," describes the mutant line made with T-DNA insertional mutations. Line S11.13-34 was described as lacking PTGS.

Example 7 describes the insertional mutation was found in SEQ ID NO:1 which was also known as At4g13870 encodes a polypeptide comprising a RNase D domain. The example further describes that the cDNA corresponding to this gene was cloned and was identified as SEQ ID NO:23. The cDNA differs from the predicted GenBank annotation. Also, the protein sequence as set forth in SEQ ID NO:24 contains a protein sequence predicted from a translation of bases 42 to 905 of the cDNA (SEQ ID NO: 23).

In view of the above comments, it is respectfully requested that this rejection be withdrawn.

Claim Rejections under 35 USC § 112, first paragraph

Claims 25-28, 38, 39, 44, 47, 58 and 59 remain and claims 51, 52 and 60 are rejected under 35 USC § 112, first paragraph as allegedly containing subject matter that was not described in the specification.

Applicants respectfully disagree. However, in order to advance prosecution of certain embodiments, the claims have been amended to delete recitation of 98%.

Examples 5 and 9 were written in the present tense. The Office Action alleges that these are prophetic examples. As argued above, the detailed results presented in Table 3 would lead one of ordinary skill in the art to realize the example 5 was actually performed due to the presence of the specific data.

Regarding Example 9, it is a prophetic example of a complementation experiment. The results of the experiments of Example 9 are set forth in the publication by Glazov et al., The Plant Journal 35:342-49 (2003), in particular, on page 345, col. 2.

Applicants respectfully point out to the Examiner that SEQ ID NO:1 is the genomic version of the gene encoding the polypeptide of SEQ ID NO:24. Also, SEQ ID NO:2 is the predicted amino acid sequence based upon the genomic clone from nucleotides 42 to 905 of SEQ ID NO:1 (Example 7, page 52).

Applicants also point out to the Examiner that the amino acid sequences of SEQ ID NO:2 and 24 are virtually identical. The amino acid sequences align from amino acids 1-277. As explained in Example 7, SEQ ID NO:24 is the amino acid sequence predicted from the cDNA clone SEQ ID NO:23 which is the RNA transcribed from the genomic gene of SEQ ID NO:1. Thus, SEQ ID NO:2 and 24 are almost the same polypeptide amino acid sequence except for after amino acid #277 (See sequence comparison attached as Exhibit A).

Thus, the description of the insertional mutation in the genomic copy of the gene of sequence SEQ ID NO:1, is therefore, an insertional mutation into the gene encoding SEQ ID NO:2 and 24.

Further, the work published in Glazov et al., does clearly describe the work of the present invention. The article is published by the same individuals as named as inventors on the present patent application. Further, the wex cDNA described in the publication (deposited as AF531179) is the same nucleotide sequence of SEQ ID NO:23 as can be observed by doing a sequence alignment (attached as Exhibit B).

The Examiner also contends on page 6, that "only one chromosomal copy of the endogeous nucleotide sequence . . . will not suffice to increase expression of a nucleotide sequence of interest. The T-DNA insert must be present in all copies."

To advance prosecution of certain embodiments of the present invention, the claims have been amended to recite the plant showing increased gene expression in homozygous for the mutated gene of the invention.

Therefore, the specification as filed, contains an enabling description of the claimed invention for those of skill in the art, and applicants request withdrawal of this rejection.

Respectfully submitted,

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